

09433360 Results

SEQ ID NO: 2

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1819	100.0	350	20	AAY57290	Human BGCKr protei
2	1819	100.0	350	20	AAY17435	Human signal pepti
3	1819	100.0	350	20	AAW93169	Human HFIAO41 prot
4	1819	100.0	350	21	AAY94325	Human seven transm
5	1819	100.0	350	22	AAG80119	Human CCR11 protei
6	1819	100.0	350	22	AAU08994	Human G protein-co
7	1819	100.0	350	22	AAG67237	Amino acid sequenc
8	1819	100.0	382	22	AAB62389	Human chemokine re
9	1814	99.7	349	20	AAW93170	Human HFIAO41 prot
10	1814	99.7	350	20	AAY30125	A human seven-pass
11	1810	99.5	350	21	AAY71301	Human orphan G pro
12	1810	99.5	350	21	AAB02835	Human G protein co
13	1808	99.4	350	21	AAB37788	Human TSC7. Homo
14	1728	95.0	333	20	AAY57289	Human BGCKr partia
15	1620	89.1	350	22	AAG67238	Amino acid sequenc
16	1591	87.5	350	20	AAY57291	Mouse BGCKr protei
17	1275	70.1	246	20	AAY57292	Human BGCKr protei
18	1257	69.1	242	22	AAM99949	Human expressed po
19	1212	66.6	263	20	AAY30126	A seven-pass trans
20	862	47.4	164	22	ABB11162	Human orphan GPCR
21	862	47.4	164	22	AAM79310	Human protein SEQ
22	824	45.3	159	21	AAB41786	Human ORFX ORF1550
23	761	41.8	175	22	AAM99976	Human expressed po
24	761	41.8	175	22	ABB10276	Human cDNA SEQ ID
25	761	41.8	175	22	AAU18115	Novel human uterin
26	761	41.8	175	22	AAU18361	Human endocrine po
27	761	41.8	175	22	AAU18669	Renal and cardiova
28	761	41.8	175	22	AAU21655	Novel human neopla
29	659	36.2	358	15	AAR53745	Partial sequence o
30	659	36.2	358	21	AAB21689	Human 7TM receptor
31	659	36.2	378	19	AAW48724	Human V31 seven tr
32	659	36.2	378	21	AAB21688	Human 7TM receptor
33	659	36.2	378	22	AAG80114	Human CCR7 protein
34	659	36.2	378	22	AAB50859	Human CCR7. Homo
35	659	36.2	410	15	AAR53743	Putative seven tra
36	659	36.2	410	19	AAW48723	Polypeptide sequen
37	659	36.2	410	21	AAB21687	Genomic clone of 7
38	659	36.2	569	22	ABG12373	Novel human diagno
39	656	36.1	378	15	AAR53744	Putative seven tra
40	655	36.0	378	21	AAY90663	Human mutant G pro
41	653	35.9	378	21	AAY90629	Human G protein-co
42	650	35.7	378	21	AAB21699	7TM receptor prote
43	643	35.3	369	22	AAG80116	Human CCR9a protei
44	643	35.3	378	15	AAR54079	Epstein Barr virus
45	643	35.3	378	19	AAW56164	G-protein coupled

Issued:

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1819	100.0	350	2	US-08-966-316-16	Sequence 16, Appl
2	1620	89.1	350	2	US-08-966-316-18	Sequence 18, Appl
3	659	36.2	358	1	US-08-153-848-19	Sequence 19, Appl
4	659	36.2	358	3	US-09-299-843A-19	Sequence 19, Appl
5	659	36.2	358	4	US-09-088-337B-19	Sequence 19, Appl
6	659	36.2	358	5	PCT-US93-11153-19	Sequence 19, Appl

7	659	36.2	378	1	US-08-153-848-15	Sequence 15, Appl
8	659	36.2	378	3	US-09-299-843A-15	Sequence 15, Appl
9	659	36.2	378	4	US-09-251-545-1	Sequence 1, Appli
10	659	36.2	378	4	US-09-088-337B-15	Sequence 15, Appl
11	659	36.2	378	5	PCT-US93-11153-15	Sequence 15, Appl
12	659	36.2	410	1	US-08-153-848-7	Sequence 7, Appli
13	659	36.2	410	3	US-09-299-843A-7	Sequence 7, Appli
14	659	36.2	410	4	US-09-088-337B-7	Sequence 7, Appli
15	659	36.2	410	5	PCT-US93-11153-7	Sequence 7, Appli
16	650	35.7	378	3	US-09-299-843A-66	Sequence 66, Appl
17	650	35.7	378	4	US-09-088-337B-66	Sequence 66, Appl
18	643	35.3	378	1	US-08-383-750-2	Sequence 2, Appli
19	643	35.3	378	1	US-08-383-751A-2	Sequence 2, Appli
20	643	35.3	378	3	US-08-352-678-2	Sequence 2, Appli
21	643	35.3	378	4	US-09-045-583-49	Sequence 49, Appl
22	643	35.3	378	5	PCT-US93-09636-2	Sequence 2, Appli
23	637	35.0	357	4	US-09-266-464-2	Sequence 2, Appli
24	635.5	34.9	359	1	US-08-153-848-24	Sequence 24, Appl
25	635.5	34.9	359	3	US-09-299-843A-24	Sequence 24, Appl
26	635.5	34.9	359	4	US-09-088-337B-24	Sequence 24, Appl
27	635.5	34.9	359	5	PCT-US93-11153-24	Sequence 24, Appl
28	606.5	33.3	361	2	US-08-902-294-2	Sequence 2, Appli
29	606.5	33.3	361	3	US-09-178-637-2	Sequence 2, Appli
30	583	32.1	374	4	US-09-045-583-48	Sequence 48, Appl
31	581	31.9	342	4	US-09-116-498-4	Sequence 4, Appli
32	569	31.3	342	4	US-09-116-498-6	Sequence 6, Appli
33	560	30.8	342	2	US-08-742-011-2	Sequence 2, Appli
34	560	30.8	342	4	US-09-275-384B-5	Sequence 5, Appli
35	560	30.8	342	4	US-09-116-498-2	Sequence 2, Appli
36	560	30.8	342	4	US-09-449-437A-2	Sequence 2, Appli
37	537.5	29.5	360	4	US-08-875-573-20	Sequence 20, Appl
38	537.5	29.5	360	4	US-09-232-878-2	Sequence 2, Appli
39	537.5	29.5	360	4	US-09-045-583-55	Sequence 55, Appl
40	534.5	29.4	355	1	US-07-759-568-1	Sequence 1, Appli
41	534.5	29.4	355	1	US-08-450-393A-8	Sequence 8, Appli
42	534.5	29.4	355	2	US-08-390-000A-5	Sequence 5, Appli
43	534.5	29.4	355	4	US-08-446-669-8	Sequence 8, Appli
44	534.5	29.4	355	5	PCT-US95-00476-8	Sequence 8, Appli
45	534.5	29.4	360	1	US-08-202-056-7	Sequence 7, Appli

RESULT 1

US-08-966-316-16

; Sequence 16, Application US/08966316

; Patent No. 5932445

; GENERAL INFORMATION:

; APPLICANT: Lal, Preeti

; APPLICANT: Au-Young, Janice

; APPLICANT: Reddy, Roopa

; APPLICANT: Murry, Lynn E.

; APPLICANT: Mathur, Preete

; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/966,316

; FILING DATE: Herewith

; CLASSIFICATION: 435

Sdo copy B

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0424 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: UTRSNOT11
; CLONE: 2547002
US-08-966-316-16

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Query Match          100.0%; Score 1819; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 7.6e-148;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MALEQNQSTDYYYEENEMNGTYDYSQYELICKEDVREFAKVFLPVFLTIVFVIGLAGNS 60
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Db 1 MALEQNQSTDYYYEENEMNGTYDYSQYELICKEDVREFAKVFLPVFLTIVFVIGLAGNS 60

Qy 61 MVVAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWLKGIMCKITSALYT 120
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 MVVAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWLKGIMCKITSALYT 120

Qy 121 LNFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWIICFCVWMAAILLSIPQLVFYTVND 180
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 LNFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWIICFCVWMAAILLSIPQLVFYTVND 180

Qy 181 NARCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKMPNIKISRPLK 240
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 NARCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKMPNIKISRPLK 240

Qy 241 VLLTVVIVFIQTLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTESIALFHSCINP 300
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 VLLTVVIVFIQTLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTESIALFHSCINP 300

Qy 301 ILYVFMGASFKNYVMKVAKKYGSWRRQRQSVVEEFPFDSEGPTPTSTFSI 350
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 ILYVFMGASFKNYVMKVAKKYGSWRRQRQSVVEEFPFDSEGPTPTSTFSI 350

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RESULT 2
US-08-966-316-18
; Sequence 18, Application US/08966316
; Patent No. 5932445
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Au-Young, Janice
; APPLICANT: Reddy, Roopa
; APPLICANT: Murry, Lynn E.
; APPLICANT: Mathur, Preete
; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA

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; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/966,316
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0424 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 399711
US-08-966-316-18

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Query Match          89.1%; Score 1620; DB 2; Length 350;
Best Local Similarity 86.0%; Pred. No. 7.1e-131;
Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

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Qy      1 MALEQNQSTDYYYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS 60
      ||:| ||||| ||||| ||:| ||||| :||| :||| ||||| || || :||| |||||
Db      1 MAVEYNQSTDYYYEENEMNDTHDYSQYEVICIKKEVRKFAKVFLPAFFTIAFIIGLAGNS 60

Qy     61 MVVAIYAYYKKQRTKTDVYIILNLAVADLLLLFTLPFWAVNAVHGWLKGIMCKITSALYT 120
      ||||| ||||| :||| ||||| ||||| ||||| ||||| ||||| :||| |||||
Db     61 TVVAIYAYYKKRRTKTDVYIILNLAVADLFLFTLPFWAVNAVHGWLKGIMCKVTSALYT 120

Qy    121 LNFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWIIICFCVWMAAILLSIPQLVFYTVND 180
      :||| ||||| ||||| || || ||||| ||||| :||| :||| ||||| |||||
Db    121 VNFVSGMQFLACISTDRYWAVTKAPSQSGVGKPCWVICFCVWVAAAILLSIPQLVFYTVNH 180

Qy    181 NARCIPIFPYRLGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKMPNIKISRPLK 240
      |||: |||| :||| |||| ||: ||||| :||| ||||| :||| ||||| :|||
Db    181 KARCVPFPYHLGTSMKASIQLEICIGFIIPFLIMAVCYFITAKTLIKMPNIKKSQPLK 240

Qy    241 VLLTVVIVFIVTQLPYNIVKFCRAIDIYSLITSCNMSKRMDIAIQVTESIALFHSCCLNP 300
      || ||||| ||||| ||||| :||| ||||| ||: ||||| :||| ||||| |||||
Db    241 VLFTVVIVFIVTQLPYNIVKFCQAIDIYSLITDCMSKRMDVAIQITESIALFHSCCLNP 300

Qy    301 ILYVFMGASFKNYVMKVAKKYGSWRRQRQSVVEFPDSEGPTEPTSTFSI 350
      :||| ||||| ||||| :||| ||||| ||||| ||||| ||||| |||||
Db    301 VLYVFMGTSFKNYIMKVAKKYGSWRRQRQNVVEIPFESEDATEPTSTFSI 350

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SUMMARIES

Result	Query						
No.	Score	Match	Length	DB	ID	Description	

1	1620	89.1	350	2	JN0621	G protein-coupled
2	659	36.2	378	2	B55735	lymphocyte-specifi
3	650	35.7	378	2	A55735	G protein-coupled
4	643	35.3	378	2	A45680	G protein-coupled
5	583	32.1	369	2	JC5068	G protein-coupled
6	537.5	29.5	360	2	A57160	chemokine (C-C) re
7	534.5	29.4	360	2	A53611	interleukin-8 rece
8	524	28.8	354	2	I58186	probable G protein
9	522.5	28.7	355	2	JC4304	orphan G protein-c
10	522.5	28.7	360	2	JC4587	chemokine (C-C) re
11	518.5	28.5	354	2	B55733	G protein-coupled
12	511	28.1	358	2	A53752	interleukin-8 rece
13	501.5	27.6	355	2	JQ1231	interleukin-8 rece
14	500.5	27.5	352	2	A45747	neuropeptide Y/pep
15	499.5	27.5	353	2	S28787	neuropeptide Y/pep
16	493.5	27.1	352	2	G00048	fusin (LESTRA) - c
17	492	27.0	360	2	JC2443	chemokine (C-C) re
18	489.5	26.9	350	2	A39445	interleukin-8 rece
19	486	26.7	355	2	JC5067	G protein-coupled
20	485	26.7	355	2	I49339	macrophage inflamm
21	484.5	26.6	352	2	A43113	chemokine (C-C) re
22	483.5	26.6	359	2	A48921	interleukin-8 rece
23	482	26.5	374	2	I38450	chemokine (C-C) re
24	479.5	26.4	359	2	I49341	MIP-1 alpha recept
25	476.5	26.2	367	2	JE0349	interferon-inducib
26	474	26.1	355	2	A45177	chemokine (C-C) re
27	471	25.9	356	2	S42096	interleukin-8 rece
28	470	25.8	383	2	S55594	G protein-coupled
29	461.5	25.4	355	2	G02436	chemokine (C-C) re
30	455.5	25.0	359	2	S44425	angiotensin II rec
31	452.5	24.9	359	2	JC1104	angiotensin II rec
32	452.5	24.9	359	2	JC2134	angiotensin II rec
33	450	24.7	359	2	S15403	angiotensin II rec
34	450	24.7	374	2	S32785	G protein-coupled
35	446.5	24.5	359	2	A48857	angiotensin II rec
36	445.5	24.5	356	2	I49340	MIP-1 alpha recept
37	442.5	24.3	372	2	S26667	G protein-coupled
38	442.5	24.3	374	2	S42628	G protein-coupled
39	441	24.2	362	2	JN0694	angiotensin II rec
40	439	24.1	359	2	A42656	angiotensin II rec
41	438.5	24.1	359	2	JH0621	angiotensin II rec
42	438.5	24.1	362	2	A39714	G protein-coupled
43	437.5	24.1	327	2	S56162	MDCR15 protein - h
44	434	23.9	359	2	JQ1516	angiotensin II rec
45	428.5	23.6	359	2	I39418	angiotensin II rec

RESULT 1

JN0621

G protein-coupled receptor type B - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 19-May-2000

C;Accession: JN0621

R;Matsuoka, I.; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K.

Biochem. Biophys. Res. Commun. 194, 504-511, 1993

A;Title: Identification of novel members of G-protein coupled receptor superfamily expressed in bovine taste tissue.

A;Reference number: JN0621; MUID:93326166

A;Accession: JN0621

A;Molecule type: mRNA

A;Residues: 1-350 <MAT>

A;Cross-references: GB:S63848; NID:g399710; PIDN:AAB27547.1; PID:g399711

A;Experimental source: tongue taste papillae

C;Comment: This protein is involved in modulating taste sensitivity or regeneration of taste cells.

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein

F;42-66/Domain: transmembrane #status predicted <TM1>

28	501.5	27.6	355	1	IL8A_RABIT	P21109	oryctolagus
29	501.5	27.6	358	1	CKR3_CAVPO	Q9z2i3	cavia porce
30	500.5	27.5	352	1	CCR4_HUMAN	P30991	homo sapien
31	499.5	27.5	353	1	CCR4_BOVIN	P25930	bos taurus
32	499.5	27.5	360	1	IL8B_BOVIN	Q28003	bos taurus
33	498.5	27.4	352	1	CCR4_PAPAN	P56491	papio anubi
34	498.5	27.4	352	1	CKR5_CERTO	O62743	cercocobus
35	498.5	27.4	353	1	CCR4_FELCA	P56498	felis silve
36	497.5	27.4	350	1	IL8A_GORGO	P55919	gorilla gor
37	495.5	27.2	352	1	CKR5_CERAE	P56493	cercopithec
38	494.5	27.2	352	1	CCR4_CERTO	O62747	cercocobus
39	493.5	27.1	352	1	CCR4_MACFA	Q28474	macaca fasc
40	493.5	27.1	352	1	CCR4_MACMU	P79394	macaca mula
41	492.5	27.1	359	1	CKR3_RAT	O54814	rattus norv
42	492.5	27.1	359	1	IL8B_RAT	P35407	rattus norv
43	491.5	27.0	352	1	CKR5_PAPHA	P56441	papio hamad
44	491.5	27.0	352	1	CKR5_PYGBI	O97880	pygathrix b
45	490.5	27.0	352	1	CKR5_MACMU	P79436	macaca mula

ALIGNMENTS

RESULT 1

CKRB_HUMAN

ID CKRB_HUMAN STANDARD; PRT; 350 AA.

AC Q9NPB9;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE C-C chemokine receptor type 11 (C-C CKR-11) (CC-CKR-11) (CCR-11)

DE (Chemokine receptor-like 1) (CCRL1) (CCX CKR).

GN CCR11 OR CCBP2 OR VSHK1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20200450; PubMed=10734104;

RA Schweickart V.L., Epp A., Raport C.J., Gray P.W.;

RT "CCR11 Is a functional receptor for the monocyte chemoattractant

protein family of chemokines.";

RL J. Biol. Chem. 275:9550-9556(2000).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=20171478; PubMed=10706668;

RA Gosling J., Dairaghi D.J., Wang Y., Hanley M., Talbot D., Miao Z.,

Schall T.J.;

RT "Cutting edge: identification of a novel chemokine receptor that binds

dendritic cell- and T cell-active chemokines including ELC, SLC, and

TECK.";

RL J. Immunol. 164:2851-2856(2000).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=20231748; PubMed=10767544;

RA Khoja H., Wang G., Ng C.-T.L., Tucker J., Brown T., Shyamala V.;

RT "Cloning of CCRL1, an orphan seven transmembrane receptor related to

chemokine receptors, expressed abundantly in heart.";

RL Gene 246:229-238(2000).

CC -!- FUNCTION: RECEPTOR FOR SCYA2/MCP1, SCYA8/MCP2, SCYA13/MCP4.

CC SCYA19/MIP3B/ELC, SCYA21/SLC AND SCYA25/TECK.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN HEART. LOWER

EXPRESSION IN LUNG, PANCREAS, SPLEEN, SMALL INTESTINE AND FETAL

TISSUES.

CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

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DR EMBL; AF193507; AAF61299.1; -.
DR EMBL; AF233281; AAF44751.1; -.
DR EMBL; AF110640; AAF59827.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 43 63 POTENTIAL.
FT DOMAIN 64 87 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 88 108 POTENTIAL.
FT DOMAIN 109 113 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 114 134 POTENTIAL.
FT DOMAIN 135 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 175 POTENTIAL.
FT DOMAIN 176 201 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 202 222 POTENTIAL.
FT DOMAIN 223 240 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 241 261 POTENTIAL.
FT DOMAIN 262 289 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 290 310 POTENTIAL.
FT DOMAIN 311 350 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 112 184 BY SIMILARITY.
SQ SEQUENCE 350 AA; 39913 MW; 8E26049D2D5757C8 CRC64;

```

Qy	1	MALEQNQSTDYYYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS	60
Db	1	MALEQNQSTDYYYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS	60
Qy	61	MVVAIYAYYKKQRTKTDVYII LNLA VADLLLFTLPFWAVNAVHGWL GKIMCKITSALYT	120
Db	61	MVVAIYAYYKKQRTKTDVYII LNLA VADLLLFTLPFWAVNAVHGWL GKIMCKITSALYT	120
Qy	121	LNFVSGMQFLACISIDRYVA VKPVS QSGVG KPCWII CFCVWMAAILLSIPQLVFYTVND	180
Db	121	LNFVSGMQFLACISIDRYVA VKPVS QSGVG KPCWII CFCVWMAAILLSIPQLVFYTVND	180
Qy	181	NARCIPIFP RYLGTSMKALI QMLEICIGFVP PFLIMGVCYFITARTLMKMPNIKISRPLK	240
Db	181	NARCIPIFP RYLGTSMKALI QMLEICIGFVP PFLIMGVCYFITARTLMKMPNIKISRPLK	240
Qy	241	VLLTVVIVFI VTQLPYNI VKFCRAIDI IYSLITSCNMSKRMDIAIQVTESIALFH SCLNP	300
Db	241	VLLTVVIVFI VTQLPYNI VKFCRAIDI IYSLITSCNMSKRMDIAIQVTESIALFH SCLNP	300
Qy	301	ILYVFMGASFKNYVMKVAKKYGS WRRRQRQSVEEFPFDSEGPTEPTSTFSI	350
Db	301	ILYVFMGASFKNYVMKVAKKYGS WRRRQRQSVEEFPFDSEGPTEPTSTFSI	350

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 11 (C-C CKR-11) (CC-CKR-11) (CCR-11)
DE (Possible gustatory receptor type B) (PPR1 protein).
GN CCR11.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tongue;
RX MEDLINE=93326166; PubMed=8392843;
RA Matsuoka I., Mori T., Aoki J., Sato T., Kurihara K.;
RT "Identification of novel members of G-protein coupled receptor
RT superfamily expressed in bovine taste tissue."
RL Biochem. Biophys. Res. Commun. 194:504-511(1993).
CC -!- FUNCTION: RECEPTOR FOR SCYA2/MCP1, SCYA8/MCP2, SCYA13/MCP4.
CC SCYA19/MIP3B/ELC, SCYA21/SLC AND SCYA25/TECK (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN CIRCUMVALLATE AND FUNGIFORM
CC PAPILLAE, OLFACTORY EPITHELIUM AND LUNG. LOWER EXPRESSION IN
CC LIVER, KIDNEY AND TONGUE EPITHELIUM BEARING NO TASTE PAPILLAE.
CC VERY LOW EXPRESSION IN THE CEREBRAL CORTEX OF THE BRAIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; S63848; AAB27547.1; -.
DR PIR; JN0621; JN0621.
DR GCRDb; GCR_0757; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation.
FT DOMAIN 1 41 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 42 66 1 (POTENTIAL).
FT DOMAIN 67 79 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 80 99 2 (POTENTIAL).
FT DOMAIN 100 113 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 114 135 3 (POTENTIAL).
FT DOMAIN 136 153 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 154 175 4 (POTENTIAL).
FT DOMAIN 176 199 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 200 222 5 (POTENTIAL).
FT DOMAIN 223 241 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 242 265 6 (POTENTIAL).
FT DOMAIN 266 283 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 284 306 7 (POTENTIAL).
FT DOMAIN 307 350 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 112 184 BY SIMILARITY.
SQ SEQUENCE 350 AA; 40008 MW; E46BF942F3919C82 CRC64;

Query Match 89.1%; Score 1620; DB 1; Length 350;
Best Local Similarity 86.0%; Pred. No. 1.8e-92;
Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

Qy 1 MALEQNQSTDYYYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS 60
| | : | | | | | | | | | | : | | | | : | | | | : | | | | | | | | | | | | | | | | |



Db 1 MAVEYNQSTDYYYEENEMNDTHDYSQYEVICIKKEVRKFAKVFLPAFFTIAFIIGLAGNS 60

Qy 61 MVVAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGVLGKIMCKITSALYT 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 TVVAIYAYYKKRRTKTDVYILNLAVADLFLFTLPFWAVNAVHGVLGKIMCKVTSALYT 120

Qy 121 LNFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWIIFCFVWMAAILLSIPQLVFTVND 180
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 121 VNFVSGMQFLACISTDRYWAVTKAPSQSGVGKPCWICFCFVWMAAILLSIPQLVFTVNH 180

Qy 181 NARCIPIFPRYLGTSMKALIQLLEICIGFVVPFLIMGVCFITARTLMKMPNIKISRPLK 240
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 181 KARCVPFIPYHLGTSMKASIQILEICIGFIIPFLIMAVCFITAKTLIKMPNIKKSQPLK 240

Qy 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMEDIAIQVTESIALFHSCINP 300
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 241 VLFTVVIVFIVTQLPYNIVKFCQAIDIIYSLITDCDMSKRMVAIQITESIALFHSCINP 300

Qy 301 ILYVFMGASFKNYVMKVAKKYGSWRRQRQSVVEFPFDSEGPTEPTSTFSI 350
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 301 VLYVFMGTSFKNYIMKVAKKYGSWRRQRQNVVEIPFESEDATEPTSTFSI 350

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1596	87.7	350	11	Q924I3	Q924i3 mus musculu
2	912	50.1	221	11	Q9ESK1	Q9eskl rattus norv
3	643	35.3	369	4	Q9UQQ6	Q9uqq6 homo sapien
4	611	33.6	367	11	Q9R1V0	Q9rlv0 mus musculu
5	586.5	32.2	368	13	O42444	O42444 oncorhynch
6	578	31.8	343	6	Q9N0Z0	Q9n0z0 cercocobus
7	566.5	31.1	351	11	Q9EQ16	Q9eq16 mus musculu
8	566	31.1	343	6	Q9BDS6	Q9bds6 macaca fasc
9	561.5	30.9	351	11	Q9ERH5	Q9erh5 mus musculu
10	560	30.8	342	4	Q9HCA5	Q9hca5 homo sapien
11	559	30.7	342	6	Q9TV16	Q9tv16 pan troglod
12	544	29.9	358	13	Q9PUA0	Q9pua0 acipenser r
13	534.5	29.4	360	11	Q91ZH4	Q91zh4 rattus norv
14	527	29.0	384	4	Q96A02	Q96a02 homo sapien
15	520.5	28.6	358	13	Q9YGC3	Q9ygc3 xenopus lae
16	516	28.4	355	11	Q9JLY8	Q9jly8 rattus norv
17	507.5	27.9	347	6	Q9M2M1	Q9mzm1 eulemur mac
18	507	27.9	357	13	O42445	O42445 oncorhynch
19	506.5	27.8	347	6	Q9M2M7	Q9mzm7 callimico g
20	506.5	27.8	347	6	Q9M2M6	Q9mzm6 callicebus
21	503.5	27.7	347	6	Q9M2N0	Q9mzn0 alouatta se
22	503.5	27.7	352	6	Q9TV44	Q9tv44 cercopithec
23	502.5	27.6	347	6	Q9M2P1	Q9mzp1 mandrillus
24	502.5	27.6	347	6	Q9M2M9	Q9mzm9 ateles pani
25	502.5	27.6	347	6	Q9M2M8	Q9mzm8 callithrix
26	502.5	27.6	347	6	Q9M2M5	Q9mzm5 pithecia pi
27	500.5	27.5	347	6	Q9M2P6	Q9mzp6 presbytis j
28	500.5	27.5	347	6	Q9M2N6	Q9mzn6 hylobates c
29	500.5	27.5	347	6	Q9M2N5	Q9mzn5 hylobates h
30	500.5	27.5	347	6	Q9M2N2	Q9mzn2 pongo pygma
31	500.5	27.5	347	6	Q9M2N1	Q9mzn1 gorilla gor
32	500.5	27.5	352	6	Q9TSQ8	Q9tsq8 cercopithec
33	499.5	27.5	339	6	Q9TUR8	Q9tur8 cercopithec
34	499.5	27.5	339	6	Q9TUR4	Q9tur4 mandrillus
35	499.5	27.5	347	6	Q9M2Q3	Q9mzq3 pygathrix a
36	499.5	27.5	347	6	Q9M2Q2	Q9mzq2 rhinopithec
37	499.5	27.5	347	6	Q9M2Q1	Q9mzq1 pygathrix b
38	499.5	27.5	347	6	Q9M2Q0	Q9mzq0 pygathrix n
39	499.5	27.5	347	6	Q9M2P9	Q9mzp9 nasalis lar
40	499.5	27.5	347	6	Q9M2P8	Q9mzp8 colobus pol
41	499.5	27.5	347	6	Q9M2P5	Q9mzp5 presbytis p
42	499.5	27.5	347	6	Q9M2P4	Q9mzp4 presbytis f

43	499.5	27.5	347	6	Q9MZP3	Q9mzp3 presbytis e
44	499.5	27.5	347	6	Q9MZP2	Q9mzp2 mandrillus
45	499.5	27.5	347	6	Q9MZP0	Q9mzp0 macaca assa

ALIGNMENTS

RESULT 1
Q924I3
ID Q924I3 PRELIMINARY; PRT; 350 AA.
AC Q924I3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CHEMOKINE RECEPTOR CCR11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=20519697; PubMed=11063828;
RA Dorf M.E., Berman M.A., Tanabe S., Heesen M., Luo Y.;
RT "Astrocytes express functional chemokine receptors."
RL J. Neuroimmunol. 111:109-121(2000).
DR EMBL; AF306532; AAK81712.1; -.
KW Receptor.
SQ SEQUENCE 350 AA; 39530 MW; C5F7D9DC949CECCF CRC64;

Query Match 87.7%; Score 1596; DB 11; Length 350;
Best Local Similarity 85.4%; Pred. No. 1.6e-133;
Matches 299; Conservative 26; Mismatches 25; Indels 0; Gaps 0;

Qy	1	MALEQNQSTDYYYEENEMNGTYDYSQVELICKEDVREFAKVFLPVFLTIVFVIGLAGNS	60
Db	1	MALELNQSAEYYYEENEMNYTHDYSQVEVICIKEEVRQFAKVFLPAFFTVAFVTGLAGNS	60
Qy	61	MVVAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWLKIMCKITSALYT	120
Db	61	VVVAIYAYYKKQRTKTDVYILNLAVADLLLLITLPFWAVNAVHGWLKMMCKVTSALYT	120
Qy	121	LNFBVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWIIICFVWMAAILLSIPQLVFYTVND	180
Db	121	VNFVSGMQFLACISIDRYWAITKAPSQSGAGRPCWIIICCVWMAAILLSIPQLVFYTVNQ	180
Qy	181	NARCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKMPNIKISRPLK	240
Db	181	NARCTPIFPHHLGTSLKASIQMLEIGIGFVVPFLIMGVCYASTARALIKMPNIKKSRPLR	240
Qy	241	VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSLNLP	300
Db	241	VLLAVVVVIVTQLPYNVVKFCQAIDAIYLLITSCDMSKRMDVAIQVTESIALFHSLNLP	300
Qy	301	ILYVFMGASFKNYVMKVAKKYGSWRRQRQSVEEFPFDSEGPTPTSTFSI	350
Db	301	ILYVFMGASFKNYIMKVAKKYGSWRRQRQNVVEIIPFDSEGPTPTSSFTI	350

SEQ ID NO: 1

SUMMARIES

Result	No.	Score	% Match	Length	DB	ID	Description
	1	1915	97.8	1915	9	AF110640	AF110640 Homo sapi
c	2	1827.8	93.4	170546	2	AC074296	AC074296 Homo sapi

	3	1827.8	93.4	178159	9	HSJ509I19	AL121834 Human DNA
c	4	1825.8	93.2	162029	9	AC020632	AC020632 Homo sapi
	5	1813.8	92.6	2407	6	E30057	E30057 G protein c
	6	1799.8	91.9	2156	6	E30058	E30058 G protein c
	7	1671.4	85.4	1925	6	AX244232	AX244232 Sequence
	8	1671.4	85.4	1925	9	AF193507	AF193507 Homo sapi
	9	1574.6	80.4	1839	6	AX244231	AX244231 Sequence
	10	1462.6	74.7	1637	6	AX041923	AX041923 Sequence
	11	1370.8	70.0	1388	6	AX244225	AX244225 Sequence
	12	1150	58.7	1150	6	AX244230	AX244230 Sequence
	13	1132	57.8	1147	6	AX113671	AX113671 Sequence
	14	1132	57.8	1147	6	AX203742	AX203742 Sequence
	15	1119.2	57.2	1147	6	AX113673	AX113673 Sequence
	16	1111.4	56.8	1113	6	AX239641	AX239641 Sequence
	17	1111.4	56.8	1113	9	AF233281	AF233281 Homo sapi
	18	1051.4	53.7	1053	6	AX239643	AX239643 Sequence
	19	1051.4	53.7	1053	6	AX244219	AX244219 Sequence
	20	961.2	49.1	2059	4	S63848	S63848 G-protein c
	21	961.2	49.1	2059	6	AX244221	AX244221 Sequence
	22	831	42.4	831	6	AX244223	AX244223 Sequence
	23	797	40.7	797	6	AX244229	AX244229 Sequence
	24	790.4	40.4	1138	10	AF306532	AF306532 Mus muscu
	25	604	30.8	604	6	AX244227	AX244227 Sequence
	26	481	24.6	481	6	AX244224	AX244224 Sequence
	27	447.4	22.8	665	10	AF090348	AF090348 Rattus no
	28	374	19.1	374	6	AX244228	AX244228 Sequence
	29	345.4	17.6	347	6	AX113681	AX113681 Sequence
	30	180.2	9.2	1631	10	AF121670	AF121670 Rattus no
	31	169.2	8.6	1302	10	AB009369	AB009369 Mus muscu
	32	169.2	8.6	1674	10	MSM222714	AJ222714 Mus muscu
	33	166.2	8.5	1500	9	HSDNABLR2	X84702 H.sapiens B
	34	166.2	8.5	1900	6	AR107241	AR107241 Sequence
	35	166.2	8.5	2058	6	AR107232	AR107232 Sequence
	36	166.2	8.5	2139	9	HUMEBI1CDN	L31581 Human G pro
	37	166.2	8.5	2160	6	AR107239	AR107239 Sequence
	38	166.2	8.5	2215	9	HUMEBI103	L31584 Human G pro
c	39	166.2	8.5	133801	9	AC004585	AC004585 Homo sapi
	40	166	8.5	1410	10	AB016031	AB016031 Mus muscu
	41	164.8	8.4	1186	9	HS132337	AJ132337 Homo sapi
	42	164.8	8.4	2462	9	AF145440	AF145440 Homo sapi
	43	164.8	8.4	2544	9	AF145439	AF145439 Homo sapi
	44	164.8	8.4	2577	9	HSU45982	U45982 Human G pro
c	45	164.8	8.4	176968	9	AC005669	AC005669 Homo sapi

SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
	1	1958	100.0	1958	21	AAA27006
	2	1813.8	92.6	2407	20	AAX22557
	3	1800	91.9	1800	24	AAS98075
	4	1799.8	91.9	2156	20	AAX22558
	5	1671.4	85.4	1925	22	AAH77722
	6	1636.8	83.6	1660	20	AAX61288
	7	1574.6	80.4	1839	22	AAH77721
	8	1462.6	74.7	1637	21	AAC68722
	9	1370.8	70.0	1388	22	AAH77715
	10	1207.4	61.7	1232	20	AAZ90528
	11	1150	58.7	1150	22	AAH77720
	12	1145.8	58.5	1150	20	AAX86674
	13	1132	57.8	1147	22	AAF57685
	14	1119.2	57.2	1147	22	AAF57686
	15	1111.4	56.8	1113	22	AAS14572
	16	1090	55.7	1130	20	AAZ90527
c	17	1057.4	54.0	1059	24	AAS98091
	18	1051.4	53.7	1053	22	AAH77711
	19	1041.8	53.2	1053	21	AAD01128
	20	1041.8	53.2	1053	21	AAA46029

21	996.8	50.9	1001	21	AAC75995	Human ORFX ORF1550
22	961.2	49.1	2059	22	AAH77712	Nucleotide sequenc
23	831	42.4	831	22	AAH77713	EST related to hum
24	816	41.7	828	22	AAI99561	Human expressed po
25	797	40.7	797	22	AAH77719	Nucleotide sequenc
26	770.4	39.3	1053	20	AAZ90529	Mouse BGCKr protei
27	652	33.3	660	24	AAS98119	Human DNA for pote
28	604	30.8	604	22	AAH77717	Nucleotide sequenc
29	592.2	30.2	789	20	AAX86675	DNA encoding a sev
c 30	551.6	28.2	821	22	AAI99588	Human expressed po
c 31	551.6	28.2	821	22	ABA06498	Human cDNA SEQ ID
c 32	551.6	28.2	821	22	AAS28957	cDNA encoding for
c 33	551.6	28.2	821	22	AAS29590	Human endocrine po
c 34	551.6	28.2	821	22	AAS30190	DNA encoding rena
c 35	551.6	28.2	821	22	AAS34854	cDNA encoding nove
36	493	25.2	493	22	ABA08406	Human orphan GPCR
37	493	25.2	493	22	AAK52443	Human polynucleoti
38	481	24.6	481	22	AAH77714	Nucleotide sequenc
39	374	19.1	374	22	AAH77718	Nucleotide sequenc
40	225	11.5	415	22	AAK51459	Human polynucleoti
41	167.8	8.6	2160	15	AAQ66160	Putative seven tra
42	166.2	8.5	1137	21	AAA30632	Human G protein-co
43	166.2	8.5	1137	21	AAA30729	DNA encoding human
44	166.2	8.5	1710	23	AAS76560	DNA encoding novel
45	166.2	8.5	1900	15	AAQ66162	Partial coding seq

Issued:

SUMMARIES						
Result	% Query					
No.	Score	Match Length DB	ID	Description		
1	1636.8	83.6	1660	2	US-08-966-316-17	Sequence 17, Appl
2	166.2	8.5	1900	1	US-08-153-848-18	Sequence 18, Appl
3	166.2	8.5	1900	3	US-09-299-843A-18	Sequence 18, Appl
4	166.2	8.5	1900	4	US-09-088-337B-18	Sequence 18, Appl
5	166.2	8.5	1900	5	PCT-US93-11153-18	Sequence 18, Appl
6	166.2	8.5	2058	1	US-08-153-848-6	Sequence 6, Appli
7	166.2	8.5	2058	3	US-09-299-843A-6	Sequence 6, Appli
8	166.2	8.5	2058	4	US-09-088-337B-6	Sequence 6, Appli
9	166.2	8.5	2058	5	PCT-US93-11153-6	Sequence 6, Appli
10	166.2	8.5	2160	1	US-08-153-848-14	Sequence 14, Appl
11	166.2	8.5	2160	3	US-09-299-843A-14	Sequence 14, Appl
12	166.2	8.5	2160	4	US-09-088-337B-14	Sequence 14, Appl
13	166.2	8.5	2160	5	PCT-US93-11153-14	Sequence 14, Appl
14	164.8	8.4	2577	4	US-09-266-464-1	Sequence 1, Appli
15	164.6	8.4	2085	3	US-09-299-843A-65	Sequence 65, Appl
16	164.6	8.4	2085	4	US-09-088-337B-65	Sequence 65, Appl
17	159.8	8.2	2154	1	US-08-383-750-1	Sequence 1, Appli
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US-08-966-316-17
; Sequence 17, Application US/08966316
; Patent No. 5932445
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Au-Young, Janice
; APPLICANT: Reddy, Roopa
; APPLICANT: Murry, Lynn E.
; APPLICANT: Mathur, Preete
; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/966,316
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0424 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1660 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: UTRSNOT11
; CLONE: 2547002
US-08-966-316-17

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RESULT 1
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; Sequence 17, Application US/08966316
; Patent No. 5932445
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Au-Young, Janice
; APPLICANT: Reddy, Roopa
; APPLICANT: Murry, Lynn E.
; APPLICANT: Mathur, Preete
; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/966,316
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0424 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1660 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: UTRSNOT11
; CLONE: 2547002
US-08-966-316-17

Query Match 79.1%; Score 256.4; DB 2; Length 1660;
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SEQ ID NO: 1 nucleotides 652-1890

RESULT 1
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; Sequence 17, Application US/08966316
; Patent No. 5932445
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Au-Young, Janice
; APPLICANT: Reddy, Roopa
; APPLICANT: Murry, Lynn E.
; APPLICANT: Mathur, Preete
; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/966,316
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0424 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1660 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: UTRSNOT11
; CLONE: 2547002
US-08-966-316-17

Query Match 85.0%; Score 1053.4; DB 2; Length 1660;
Best Local Similarity 99.8%; Pred. No. 6.3e-254;
Matches 1065; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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